

AMENDMENTS TO THE CLAIMS:

This listing of the claims below will replace all prior versions and listing of claims in this application.

1-42. (Canceled)

43. (New) A nucleic acid molecule encoding a protein with the enzymatic activity of a class 3 branching enzyme,

wherein the class 3 branching enzyme comprises an iso-amylase domain and an alpha-amylase domain, and wherein the C-terminal end of the iso-amylase domain is separated from the N-terminal beginning of the alpha-amylase domain by at least 198 amino acids, and

wherein said protein catalyses a transglycosylation reaction, in which α -1,4 links of an α -1,4-glucan donor are hydrolysed and released, and wherein the α -1,4-glucan chains are transformed into α -1,6-links.

44. (New) A nucleic acid molecule encoding a protein with the enzymatic activity of a class 3 branching enzyme,

wherein the class 3 branching enzyme comprises an iso-amylase domain and an alpha-amylase domain, and wherein the C-terminal end of the iso-amylase domain is separated from the N-terminal beginning of the alpha-amylase domain by 150 to 198 amino acids, and

wherein said protein catalyses a transglycosylation reaction, in which α -1,4 links of an α -1,4-glucan donor are hydrolysed and released, and wherein the α -1,4-glucan chains are transformed into α -1,6-links.

45. (New) The nucleic acid molecule of claim 43, wherein the nucleic acid molecule comprises

- (a) a nucleic acid sequence encoding an amino acid sequence of SEQ ID NO: 4;
- (b) a nucleic acid sequence encoding an amino acid sequence with an identity of at least 95% with SEQ ID NO: 4;
- (c) a nucleic acid sequence comprising SEQ ID NO: 3 or a complementary sequence thereof;

(d) a nucleic acid sequence with an identity of at least 95% with the nucleic acid sequences of a) or c);

(e) a nucleic acid sequence that hybridizes with at least one strand of the nucleic acid molecule of (a) or (c) under stringent conditions, wherein said stringent conditions are conducting the hybridization reaction at 65°C-68°C in a solution comprising 2X SSC 10X Denhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml herring sperm DNA; 50 µg/ml tRNA; or 25 M sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS, and washing at 65°C-68°C in a solution comprising 0.2X SSC and 0.1% SDS; or

(f) a nucleic acid sequence which deviates from the sequence of the nucleic acid molecules identified under (a), (b), (c), (d) or (e) due to the degeneration of the genetic code.

46. (New) The nucleic acid molecule of claim 45, wherein the nucleic acid sequence encodes an amino acid sequence of SEQ ID NO: 4.

47. (New) The nucleic acid molecule of claim 45, wherein the nucleic acid sequence encodes an amino acid sequence with an identity of at least 95% with the amino acid sequence of SEQ ID NO: 4.

48. (New) The nucleic acid molecule of claim 45, wherein the nucleic acid sequence comprises SEQ ID NO: 3 or a complementary sequence thereof.

49. (New) The nucleic acid molecule of claim 45, wherein the nucleic acid molecule comprises a nucleic acid sequence with an identity of at least 95% with the nucleic acid sequences of (a) or (c).

50. (New) The nucleic acid molecule of claim 45, wherein the nucleic acid sequence hybridizes with at least one strand of the nucleic acid molecule of (a) or (c) under stringent conditions, wherein said stringent conditions are conducting the hybridization reaction at 65°C-68°C in a solution comprising 2X SSC 10X Denhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml herring sperm DNA; 50 µg/ml tRNA; or 25 M sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS, and washing at 65°C-68°C in a solution comprising 0.2X SSC and 0.1% SDS.

51. (New) The nucleic acid molecule of claim 45, wherein the nucleic acid sequence deviates from the sequence of the nucleic acid sequences of (a), (b), (c), (d) or (e) due to the degeneration of the genetic code.
52. (New) The nucleic acid molecule of claim 45, wherein the nucleic acid molecule encodes a class 3 branching enzyme of potato.
53. (New) A vector comprising the nucleic acid molecule of claim 45.
54. (New) The vector of claim 48, wherein the nucleic acid molecule is linked with regulatory sequences for transcription into prokaryotic or eukaryotic cells.
55. (New) A genetically modified host cell comprising the nucleic acid molecule of claim 45.
56. (New) A genetically modified plant cell comprising a foreign nucleic acid molecule, wherein said foreign nucleic acid comprises
- (a) a nucleic acid sequence encoding an amino acid sequence of SEQ ID NO: 4;
 - (b) a nucleic acid sequence encoding an amino acid sequence with an identity of at least 95% with SEQ ID NO: 4;
 - (c) a nucleic acid sequence comprising SEQ ID NO: 3 or a complementary sequence thereof;
 - (d) a nucleic acid sequence with an identity of at least 95% with the nucleic acid sequences of a) or c);
 - (e) a nucleic acid sequence that hybridizes with at least one strand of the nucleic acid molecule of (a) or (c) under stringent conditions, wherein said stringent conditions are conducting the hybridization reaction at 65°C-68°C in a solution comprising 2X SSC 10X Denhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml herring sperm DNA; 50 µg/ml tRNA; or 25 M sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS, and washing at 65°C-68°C in a solution comprising 0.2X SSC and 0.1% SDS;

(f) a nucleic acid sequence which deviates from the sequence of the nucleic acid molecules identified under (a), (b), (c), (d) or (e) due to the degeneration of the genetic code; or

(g) a nucleic acid sequence comprising at least 100 nucleotides of SEQ ID NO: 3,

wherein said genetically modified plant cell has a reduced activity of at least one class 3 branching enzyme and synthesizes a starch with a decreased phosphate content in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

57. (New) The genetically modified plant cell of claim 56, wherein the starch has a total phosphate content decreased by at least 10% in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

58. (New) The genetically modified plant cell of claim 56, wherein the starch has a C-6 phosphate content decreased by at least 15% in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

59. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid sequence encodes an amino acid sequence of SEQ ID NO: 4.

60. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid sequence encodes an amino acid sequence with an identity of at least 95% with the amino acid sequence of SEQ ID NO: 4.

61. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid sequence comprises SEQ ID NO: 3 or a complementary sequence thereof.

62. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid molecule comprises a nucleic acid sequence with an identity of at least 95% with the nucleic acid sequences of (a) or (c).

63. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid sequence hybridizes with at least one strand of the nucleic acid molecule of (a) or (c) under

stringent conditions, wherein said stringent conditions are conducting the hybridization reaction at 65°C-68°C in a solution comprising 2X SSC 10X Denhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml herring sperm DNA; 50 µg/ml tRNA; or 25 M sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS, and washing at 65°C-68°C in a solution comprising 0.2X SSC and 0.1% SDS.

64. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid sequence deviates from the sequence of the nucleic acid sequences of (a), (b), (c), (d) or (e) due to the degeneration of the genetic code.

65. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid sequence comprises at least 100 nucleotides of SEQ ID NO: 3.

66. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid sequence comprises 100-500 nucleotides of SEQ ID NO: 3.

67. (New) The genetically modified plant cell of claim 56, wherein the nucleic acid sequence comprises at least 500 nucleotides of SEQ ID NO: 3.

68. (New) The genetically modified plant cell of claim 56, wherein said foreign nucleic acid molecule is

- a) a DNA molecule, which codes at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene encoding a class 3 branching enzyme;
- b) a DNA molecule, which by means of a co-suppression effect leads to the reduction in the expression of at least one endogenous gene encoding a class 3 branching enzyme;
- c) a DNA molecule, which codes at least one ribozyme, which splits specific transcripts of at least one endogenous gene encoding a class 3 branching enzyme;
- d) a DNA molecule, which simultaneously codes at least one antisense RNA and at least one sense RNA, wherein said antisense RNA and said sense RNA form a

double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene encoding a class 3 branching enzyme; or

- e) a nucleic acid molecule introduced by means of in vivo mutagenesis, which leads to a mutation or an insertion of a heterologous sequence in at least one endogenous gene encoding a class 3 branching enzyme, wherein the mutation or insertion effects a reduction in the expression of said gene or results in the synthesis of an inactive class 3 branching enzyme.

69. (New) The genetically modified plant cell of claim 56, wherein the plant cell is a potato plant cell.

70. (New) A plant comprising the genetically modified plant cell of claim 56.

71. (New) The plant of claim 70, wherein said plant is a starch-storing plant.

72. (New) The plant of claim 71, wherein said plant is a maize, rice, wheat, rye, oat, barley, cassava, potato, sago, mung bean, pea or sorghum plant.

73. (New) The plant of claim 72, wherein said plant is a potato plant.

74. (New) Propagation material comprising the genetically modified plant cell of claim 56.

75. (New) Harvestable plant parts comprising the genetically modified plant cell of claim 56.

76. (New) A method for manufacturing a genetically modified plant, comprising;

- a) introducing at least one foreign nucleic acid molecule into the genome of a plant cell to obtain a genetically modified plant cell, wherein the foreign nucleic acid molecule comprises
 - (i) a nucleic acid sequence encoding an amino acid sequence of SEQ ID NO: 4;
 - (ii) a nucleic acid sequence encoding an amino acid sequence with an identity of at least 95% with SEQ ID NO: 4;

- (iii) a nucleic acid sequence comprising SEQ ID NO: 3 or a complementary sequence thereof;
- (iv) a nucleic acid sequence with an identity of at least 95% with the nucleic acid sequences of (i) or (iii);
- (v) a nucleic acid sequence that hybridizes with at least one strand of the nucleic acid molecule of (i) or (iii) under stringent conditions, wherein said stringent conditions are conducting the hybridization reaction at 65°C-68°C in a solution comprising 2X SSC 10X Denhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml herring sperm DNA; 50 µg/ml tRNA; or 25 M sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS, and washing at 65°C-68°C in a solution comprising 0.2X SSC and 0.1% SDS;
- (vi) a nucleic acid sequence which deviates from the sequence of the nucleic acid molecules identified under (i), (ii), (iii), (iv), or (v) due to the degeneration of the genetic code; or
- (vii) a nucleic acid sequence comprising at least 100 nucleotides of SEQ ID NO: 3,

wherein said genetically modified plant cell has a reduced activity of at least one class 3 branching enzyme and synthesizes a starch with a decreased phosphate content in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified;

- b) regenerating a plant from the genetically modified plant cell from Step a); and
- c) optionally, producing further plants with the plants of Step b).

77. (New) The method of claim 76, wherein the starch has a total phosphate content decreased by at least 10% in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

78. (New) The method of claim 76, wherein the starch has a C-6 phosphate content decreased by at least 15% in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

79. (New) The method of claim 76, wherein the nucleic acid sequence encodes an amino acid sequence of SEQ ID NO: 4.
80. (New) The method of claim 76, wherein the nucleic acid sequence encodes an amino acid sequence with an identity of at least 95% with the amino acid sequence of SEQ ID NO: 4.
81. (New) The method of claim 76, wherein the nucleic acid sequence comprises SEQ ID NO: 3 or a complementary sequence thereof.
82. (New) The method of claim 76, wherein the nucleic acid molecule comprises a nucleic acid sequence with an identity of at least 95% with the nucleic acid sequences of (i) or (iii).
83. (New) The method of claim 76, wherein the nucleic acid sequence hybridizes with at least one strand of the nucleic acid molecule of (i) or (iii) under stringent conditions, wherein said stringent conditions are conducting the hybridization reaction at 65⁰C-68⁰C in a solution comprising 2X SSC 10X Denhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml herring sperm DNA; 50 µg/ml tRNA; or 25 M sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS, and washing at 65⁰C-68⁰C in a solution comprising 0.2X SSC and 0.1% SDS.
84. (New) The method of claim 76, wherein the nucleic acid sequence deviates from the sequence of the nucleic acid sequences of (i), (ii), (iii), (iv), or (v) due to the degeneration of the genetic code.
85. (New) The method of claim 76, wherein the nucleic acid sequence comprises at least 100 nucleotides of SEQ ID NO: 3.
86. (New) The method of claim 76, wherein the nucleic acid sequence comprises 100-500 nucleotides of SEQ ID NO: 3.
87. (New) The method of claim 76, wherein the nucleic acid sequence comprises at least 500 nucleotides of SEQ ID NO: 3.

88. (New) The method of claim 76, wherein said foreign nucleic acid molecule is
- (a) a DNA molecule, which codes at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene encoding a class 3 branching enzyme;
 - (b) a DNA molecule, which by means of a co-suppression effect leads to the reduction in the expression of at least one endogenous gene encoding a class 3 branching enzyme;
 - (c) a DNA molecule, which codes at least one ribozyme, which splits specific transcripts of at least one endogenous gene encoding a class 3 branching enzyme;
 - (d) a DNA molecule, which simultaneously codes at least one antisense RNA and at least one sense RNA, wherein said antisense RNA and said sense RNA form a double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene encoding a class 3 branching enzyme; or
 - (e) a nucleic acid molecule introduced by means of in vivo mutagenesis, which leads to a mutation or an insertion of a heterologous sequence in at least one endogenous gene encoding a class 3 branching enzyme, wherein the mutation or insertion effects a reduction in the expression of said gene or results in the synthesis of an inactive class 3 branching enzyme.
89. (New) The method of claim 76, wherein the plant is a potato plant.
90. (New) A genetically modified plant cell comprising a foreign nucleic acid molecule comprising a nucleic acid molecule encoding a protein with the enzymatic activity of a class 3 branching enzyme, wherein the class 3 branching enzyme comprises an iso-amylase domain and an alpha-amylase domain, wherein the C-terminal end of the iso-amylase domain is separated from the N-terminal beginning of the alpha-amylase domain by at least 198 amino acids, and
- wherein said genetically modified plant cell has a reduced activity of at least one class 3 branching enzyme and synthesizes a starch with a decreased phosphate content in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

91. (New) A genetically modified plant cell comprising a foreign nucleic acid molecule comprising a nucleic acid molecule encoding a protein with the enzymatic activity of a class 3 branching enzyme, wherein the class 3 branching enzyme comprises an iso-amylase domain and an alpha-amylase domain, wherein the C-terminal end of the iso-amylase domain is separated from the N-terminal beginning of the alpha-amylase domain by 150 to 198 amino acids, and

wherein said genetically modified plant cell has a reduced activity of at least one class 3 branching enzyme and synthesizes a starch with a decreased phosphate content in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

92. (New) The genetically modified plant cell of claim 90, wherein the starch has a total phosphate content decreased by at least 10% in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

93. (New) The genetically modified plant cell of claim 90, wherein the starch has a C-6 phosphate content decreased by at least 15% in comparison with starch synthesized from a corresponding wild type plant cell that has not been genetically modified.

94. (New) The genetically modified plant cell of claim 90, wherein the plant cell is a potato plant cell.